

Re-run



PCT

RAW SEQUENCE LISTING

DATE: 05/08/2002

PATENT APPLICATION: US/09/869,414

TIME: 11:02:58

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Output Set: N:\CRF3\05082002\I869414.raw

1 <110> APPLICANT: Beinkowski et al.
 2 <120> TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
 USES
 3 THEREFOR
 4 <130> FILE REFERENCE: 28341/6280M
 5 <140> CURRENT APPLICATION NUMBER: US/09/869,414
 6 <141> CURRENT FILING DATE: 2001-06-27
 7 <150> PRIOR APPLICATION NUMBER: 09/416,901
 8 <151> PRIOR FILING DATE: 1999-10-13
 9 <150> PRIOR APPLICATION NUMBER: 60/155,493
 10 <151> PRIOR FILING DATE: 1999-09-23
 11 <150> PRIOR APPLICATION NUMBER: 09/404,133
 12 <151> PRIOR FILING DATE: 1999-09-23
 13 <150> PRIOR APPLICATION NUMBER: PCT/US99/20881
 14 <151> PRIOR FILING DATE: 1999-09-23
 15 <150> PRIOR APPLICATION NUMBER: 60/101,594
 16 <151> PRIOR FILING DATE: 1998-09-24
 17 <160> NUMBER OF SEQ ID NOS: 73
 18 <170> SOFTWARE: PatentIn Ver. 2.0
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 21 <211> LENGTH: 1804
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
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 27 cgcgtagttg cgcccacccc gggaccgggg acccctgccg agcgccacgc cgacggcttg 180
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 31 accccgcact cctacataga cacgtacttt gacacagaga ggtctagcac ataccgctcc 420
 32 aagggctttg acgtcacagt gaagtacaca caaggaaact ggacgggctt cgttggggaa 480
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 36 caagcaaaca tccccaacgt tttctccatg cagatgtgtg gagccggctt gcccggttgct 720
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47 gtgtctgaaa tttccggggcc tttctcaaca gaggatgtag ccagcaactg tgtccccgct 1380
48 cagtctttga gcgagcccat tttgtggatt gtgtcctatg cgctcatgag cgtctgtgga 1440
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50 cgtgaccctg aggtcgtcaa tgatgagtc tctctggtca gacatcgctg gaaatgaata 1560
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53 gctcccagat gccttctaga ttcactgtct ttgtattctt gattttcaag ctttcaaata 1740
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57 <210> SEQ ID NO: 2

58 <211> LENGTH: 518

59 <212> TYPE: PRT

60 <213> ORGANISM: Homo sapiens

61 <400> SEQUENCE: 2

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65 20 25 30
66 Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
67 35 40 45
68 Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
69 50 55 60
70 Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
71 65 70 75 80
72 Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
73 85 90 95
74 Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
75 100 105 110
76 Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
77 115 120 125
78 Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
79 130 135 140
80 Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
81 145 150 155 160
82 Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
83 165 170 175
84 Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
85 180 185 190
86 Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
87 195 200 205
88 Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
89 210 215 220
90 Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
91 225 230 235 240
92 Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
93 245 250 255
94 Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp

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99          290          295          300
100 Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
101 305          310          315          320
102 Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
103          325          330          335
104 Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
105          340          345          350
106 Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
107          355          360          365
108 Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
109          370          375          380
110 Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
111 385          390          395          400
112 Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
113          405          410          415
114 Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
115          420          425          430
116 Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
117          435          440          445
118 Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
119          450          455          460
120 Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
121 465          470          475          480
122 Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg Cys
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136 ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
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147 gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840
148 tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 900
149 gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gtccctgat 960
150 ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt 1020
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152 atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140
153 tacaagtttg ccatctcaca gtcatccacg ggcactgtta tgggagctgt tatcatggag 1200
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172 <212> TYPE: PRT

173 <213> ORGANISM: Homo sapiens

174 <400> SEQUENCE: 4

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180      35              40              45
181 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
182      50              55              60
183 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
184      65              70              75              80
185 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
186      85              90              95
187 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
188      100             105             110
189 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
190      115             120             125
191 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
192      130             135             140
193 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
194      145             150             155             160

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195   Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
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198               180                      185                      190
199   Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
200               195                      200                      205
201   Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
202               210                      215                      220
203   Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
204   225                      230                      235                      240
205   Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
206               245                      250                      255
207   Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
208               260                      265                      270
209   Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
210               275                      280                      285
211   Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
212   290                      295                      300
213   Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
214   305                      310                      315                      320
215   Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
216               325                      330                      335
217   Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
218               340                      345                      350
219   Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
220               355                      360                      365
221   Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
222   370                      375                      380
223   Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
224   385                      390                      395                      400
225   Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
226               405                      410                      415
227   Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
228               420                      425                      430
229   Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
230   435                      440                      445
231   Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
232   450                      455                      460
233   Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
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RAW SEQUENCE LISTING ERROR SUMMARY
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VERIFICATION SUMMARY

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